

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,003

```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2013
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-758-003-1

```

```

Query Match      7.5%; Score 14; DB 1; Length 2016;
Best Local Similarity 60.5%; Pred. No. 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 CTCAAAGTCTCAGACACCAAGATCGACGATCGAGGA 536
   ||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 CCCAAAGCTCCGCTGTCAGTTCTGCACTCTCCAGGA 50

```

Search completed: February 9, 2005, 08:45:53
Job time : 0.001 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 9, 2005, 08:56:35 ; Search time 0.001 Seconds
(without alignments)
2282.742 Million cell updates/sec

Title: US-09-824-134-1
Perfect score: 3092
Sequence: 1 GTGAATCAGGCACCGAGTG.....ACAAAAAAAAAAAAAAAAAAAA 1701

Scoring table:	BLOSUM62
	Xgapop 10.0 , Xgapext 0.5
	Ygapop 10.0 , Ygapext 0.5
	Fgapop 6.0 , Fgapext 7.0
	Delop 6.0 , Delext 7.0

Searched: 1 seqs, 671 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Minimum DB seq length: 2000000000
Maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

FORC-PROCESSING: Minimum Match 0% Maximum Match 100%

Maximum Match 100%
Listing first 45 summaries

```

Command line parameters:
-MODEL=frame_n2p_model -DEV=soft -Q=US09824134.seq -DB=US09758003.psp
-SUPPLIPTS=OUT-US09824134_1.n2p.align -MINMATCH=0 -LOOCPCT=0 -LOOPEXT=0
-UNITS=bps -START=1 -END=1 -MATRIX=ploucm62 -TRANS=human40.cd1 -LIST=45
-LOCALLEN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct-norm-ext -HEADSIZE=570 -MINLEN=0 -MAXLEN=200000000 -NCPU=6
-NO_XLPA -NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FCBEXT=7 -VCBOP=10 -VCAPEXT=0.5 -DELOP=5 -DELOP=7

```

Database : US09758003 . pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	111.5	3.6	671	1	US-09-758-003-2	Sequence 2, Appli
2	47	1.5	671	1	US-09-758-003-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-758-003-2
; Sequence 2, Application US/09758003
; GENERAL INFORMATION:
; APPLICANT: BAICHWAL, VIJAY R
; HUANG, JIANING
; HSU, HAILING
; GOEDDEL, DAVID V
; TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
; TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
; ASSAYS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
;

```

, CITY: HILLSBOROUGH
, STATE: CALIFORNIA
, COUNTRY: USA
, ZIP: 94010
,
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: Patentin Release #1.0, Version #1.30
,
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/758,003
, FILING DATE: 09-Jan-2001
, CLASSIFICATION: <Unknown>
,
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 09/132,118
, FILING DATE: <Unknown>
,
, ATTORNEY/AGENT INFORMATION:
, NAME: OSMAN, RICHARD A.
, REGISTRATION NUMBER: 36,627
, REFERENCE/DOCKET NUMBER: T95-006-1
,
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (650) 343-4341
, TELEFAX: (650) 343-4342
,
, INFORMATION FOR SEQ ID NO: 2:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 671 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
,
, MOLECULE TYPE: protein
, SEQUENCE DESCRIPTION: SEQ ID NO: 2:
,
, US-09-758-003-2

```

;
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,003
; FILING DATE: 09-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/132,118
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T95-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 671 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-758-003-2

Alignment Scores:
Pred. No.: 0 Length: 671
Score: 47.00 Matches: 42
Percent Similarity: 34.86% Conservatives: 19
Best Local Similarity: 24.00% Mismatches: 76
Query Match: 1.53% Indels: 39
DB: 1 Gaps: 11

US-09-824-134-1 (1-1701) x US-09-758-003-2 (1-671)

```
Qy 1455 CTCATTGCTCTGG---CAACCATCACTG-----CCC 1426
Db 354 ValGluGluSerTrpPheAlaProSerLeuGluHisProGlnGluAsnGluProSer 373
Qy 1425 CTACTTAGAGTCTCAGAGGAGGACTCACTC---ACACAGGGGCCAAGAGCTGGACCA 1369
Db 374 LeuGlnSerLysLeuGlnAspGluAlaAsnTyrHisLeuTyrGlySerArgMetAspArg 393
Qy 1368 CGGCCAACACAGGTCTCCCCACCCGCCAGCCAT-----GCCTCTCCCCACCAC 1318
Db 394 GlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArgGluGluGluArgArg 413
Qy 1317 AGCACCCCGCTGACCTAGTGTCCAGGTCTGTCCC-----GGTGGCCTCCAA 1270
Db 414 ArgValSerHisAspPheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGlu 433
Qy 1269 GGAATGGGACAAACATCTTCTGCGCACTGCAGGG---GCACGAGAACGCCACAGT 1213
Db 434 GlyLysGlyThrValTyrSerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSer 453
Qy 1212 GGTGTGAGCA-----TGGGCTCTGGTGAAGGATGGGGG----- 1180
Db 454 GlyLeuThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGly 473
Qy 1179 ---GGTTCAATCCAGTCTCCACCTCTCTGCTGTGCTCCGATTCCTGGGCTCTGAGC 1123
Db 474 PheGlyThrArgProLeuAspProGlyThrAla-----GlyProArgVal 488
Qy 1122 TGGTCTCTCCGCTGGAGTAACAGTGTGACTGTCTCATCT---GCACAGATTCCT----- 1070
Db 489 TrpTyrArgProIleProSerHisMetProSerLeuHisAsnIleProValProGluThr 508
```

Qy 1069 TCTGTGCTGGACACGGTTCCCACT-----TTCCAACTACTCCCG 1031
Db 509 AsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuPro 523

Search completed: February 9, 2005, 08:56:37
Job time : 1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 9, 2005, 09:04:15 ; Search time 0.001 Seconds
(without alignments)
1032.192 Million cell updates/sec

Title: US-09-824-134-2
Perfect score: 1302
Sequence: 1 VNQAPECFGGILGLPKR.....RSGAMSPMNSDASTGEAS 256

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1 seqs, 2016 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=soft -Q=US09824134.p2n -DB=US09758003.seq
-SUFFIX=pto -OUT=US09824134-2.p2n.align -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6
-NO_XLPXY -NEG_SCORES=0 -LONGLOG -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : US09758003.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	111.5	8.6	2016	1 US-09-758-003-1	Sequence 1, Appli
2	48	3.7	2016	1 US-09-758-003-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-758-003-1
; Sequence 1, Application US/09758003
; GENERAL INFORMATION:
; APPLICANT: BAICHUWAL, VIJAY R
; HUANG, JIANING
; HSU, HAILING
; GOEDDEL, DAVID V
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09758.003
FILING DATE: 09-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 09/132.118
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T95-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2013
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-758-003-1
Alignment Scores:
Pred. No.: 0 Length: 2016
Score: 111.50 Matches: 28
Percent Similarity: 61.04% Conservative: 19
Best Local Similarity: 36.36% Mismatches: 27
Query Match: 8.56% Indels: 3
DB: 1 Gaps: 3
US-09-824-134-2 (1-256) x US-09-758-003-1 (1-2016)
QY 152 IleCysAspAsnValGlyAspTrpArgLeuAlaArgGlnLeuLysValSerAsp 171
DB 1768 ATCAGGAAATCTGGAAAGCACCTGGAAAACTGTCCCGTAACTGGCGTTACACAG 1827
QY 172 ThrLysIleAspSerIleGluAspArgTyrProArgAsn---LeuThrGluArgValArg 190
DB 1828 TCTCAGATTGTAATTCACCATGATGAGCGAGATGGACTGAAAGAAAGGTTTAC 1887
QY 191 GluSerLeuArgIleTrpLysAsnThrGluLys---GluAsnAlaThrValAlaHisLeu 209
DB 1888 CAGATGCTCCAAAGTGGGTGATGAGGAAGGCATAAAGGGAGCCACCGTGGGGAAGCTG 1947
QY 210 ValGlyAlaLeuArgSerCys---GlnMetAsnLeuValAlaAspLeuVal 225
DB 1948 GCCCAGGGCGCTCCACAGGTTCAGGATCGACCTTCAGCAGCTTGATT 1998
RESULT 2
US-09-758-003-1/c
; Sequence 1, Application US/09758003
; GENERAL INFORMATION:
; APPLICANT: BAICHUWAL, VIJAY R
; HUANG, JIANING
; HSU, HAILING
; GOEDDEL, DAVID V
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS

1 NUMBER OF SEQUENCES: 2
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
4 STREET: 75 DENISE DRIVE
5 CITY: HILLSBOROUGH
6 STATE: CALIFORNIA
7 COUNTRY: USA
8 ZIP: 94010
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.30
15
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/758,003
18 FILING DATE: 09-Jan-2001
19 CLASSIFICATION: <Unknown>
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 09/132,118
22 FILING DATE: <Unknown>
23 ATTORNEY/AGENT INFORMATION:
24 NAME: OSMAN, RICHARD A.
25 REGISTRATION NUMBER: 36,627
26 REFERENCE/DOCKET NUMBER: T95-006-1
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (650) 343-4341
29 TELEFAX: (650) 343-4342
30
31 INFORMATION FOR SEQ ID NO: 1:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 2016 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: double
36 TOPOLOGY: linear
37 MOLECULE TYPE: cDNA
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: 1..2013
41 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
42
43 US-09-758-003-1

Alignment Scores:
Pred. NO.: 0 Length: 2016
Score: 48.00 Matches: 26
Percent Similarity: 50.00% Conservative: 8
Best Local Similarity: 38.24% Mismatches: 26
Query Match: 3.69% Indels: 8
DB: 1 Gaps: 5

US-09-824-134-2 (1-256) x US-09-758-003-1 (1-2016)

Qy	42	ArgProLeuAlaAspProAlaMetAspPropheLeuValLeuLeuHisSerValSerSer	61
Db	1257	AGGTCTATGGAGACCCCTGGG-----TCTCTTCTCTCTC-----TCTGTGTAAGC	1210
Qy	62	SerLeuSerSerSerGluLeuThrGluLeuLysPhe-----LeuCysLeuGlyArgVal	79
Db	1209	CACATTCCTGCTGGGCTGCTGTTTCCTGCTGCTCCATCGCGCTGCCATAAGATGGTA	1150
Qy	80	ValLysArgLysLeuGlu---ArgValGlnSerGlyLeuAspLeuPheSerMetLeuLeu	98
Db	1149	GTTGGCTTCGCTCTGGAGTTTACTCTGCAGGCTGGGCTCATCTCTTGTGGGTGCTC	1090
Qy	99	GluGlnAsnAspLeuGluProGly	106
Db	1089	---CAGGGAAGGACCAACCA	1069

Search completed: February 9, 2005, 09:04:16
Job time : 1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 09:01:06 ; Search time 0.001 Seconds
(without alignments)
77.836 Million cell updates/sec

Title: US-09-824-134-2
Perfect score: 593
Sequence: 1 FEAGAAGAAGBEDLCAAF.....QEVOQARDLQNRGAMSPMS 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 671 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : US09758003.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111.5	18.8	671	1	US-09-758-003-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-758-003-2
Sequence 2, Application US/09758003
GENERAL INFORMATION:
APPLICANT: BAICHWAL, VIJAY R
HUANG, JIANING
HSU, HAILING
GOEDDEL, DAVID V
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,003
FILING DATE: 09-Jan-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLYING NUMBER: 09/132,118
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T95-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-758-003-2
Query Match 18.8%; Score 111.5; DB 1; Length 671;
Best Local Similarity 36.4%; Pred. No. 0;
Matches 28; Conservative 19; Mismatches 27; Indels 3; Gaps 3;
Qy 152 ICDNVGKDWRLAROLKVSPTKIDSIEDRYPRN-LTERVRESLRWKTEK-ENATVAHL 209
Db 590 IRENLGKHWKNCARKLGFTQSQIDIDHYERDGLKEKVKYQMLQKVMREGIKGATVGKL 649
Qy 210 VGALRSC-QMNLVADLV 225
Db 650 AQALHQC-SRIDLLSLI 666
Search completed: February 9, 2005, 09:01:07
Job time : 1 secs

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